1654

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/851,965*

DATE: 09/17/98
TIME: 14:16:23

INPUT SET: S28714.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANT: YOUNG, Andrew A.
 6                       GEDULIN, Bronislava
 7                       BEYNON, Gareth Wyn
 8
 9        (ii) TITLE OF INVENTION: METHOD FOR PREVENTING GASTRITIS
10                                 USING AMYLIN OR AMYLIN
11                                 AGONISTS
12
13        (iii) NUMBER OF SEQUENCES: 35
14
15        (iv) CORRESPONDENCE ADDRESS:
16             (A) ADDRESSEE: LYON & LYON
17             (B) STREET: 633 WEST FIFTH STREET
18             (C) CITY: LOS ANGELES
19             (D) STATE: CALIFORNIA
20             (E) COUNTRY: USA
21             (F) ZIP: 90017
22
23        (v) COMPUTER READABLE FORM:
24             (A) MEDIUM TYPE: Floppy disk
25             (B) COMPUTER: IBM PC compatible
26             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27             (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29        (vi) CURRENT APPLICATION DATA:
30             (A) APPLICATION NUMBER:  08/851,965
31             (B) FILING DATE: 06-MAY-1997
32             (C) CLASSIFICATION: Pending
33
34
35       (viii) ATTORNEY/AGENT INFORMATION:
36             (A) NAME: DUFT, BRADFORD J.
37             (B) REGISTRATION NUMBER: 32,219
38             (C) REFERENCE/DOCKET NUMBER: 224/042
39
40        (ix) TELECOMMUNICATION INFORMATION:
41             (A) TELEPHONE: 619/552-2200
42             (B) TELEFAX: 213/955-0440
43             (C) TELEX: 67-3510
44
45
46   (2) INFORMATION FOR SEQ ID NO:1:
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ENTERED

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47
48        (i) SEQUENCE CHARACTERISTICS:
49            (A) LENGTH: 37 amino acids
50            (B) TYPE: amino acid
51            (C) STRANDEDNESS: single
52            (D) TOPOLOGY: linear
53
54       (ii) MOLECULE TYPE: peptide
55
56       (ix) FEATURE:
57            (B) LOCATION: 2,7
58            (D) OTHER INFORMATION: disulfide bridge between
59                                   the Cys residues
60            (B) LOCATION: 37
61            (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
62
63
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:  1:
65
66 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
67 1               5                   10                  15
68 Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val
69             20                  25                  30
70 Gly Ser Asn Thr Tyr
71         35
72
73
74 (2) INFORMATION FOR SEQ ID NO:2:
75
76       (i) SEQUENCE CHARACTERISTICS:
77           (A) LENGTH: 36 amino acids
78           (B) TYPE: amino acid
79           (C) STRANDEDNESS: single
80           (D) TOPOLOGY: linear
81
82      (ii) MOLECULE TYPE: peptide
83
84      (ix) FEATURE:
85           (B) LOCATION: 1,6
86           (D) OTHER INFORMATION: disulfide bridge between
87                                  the Cys residues
88           (B) LOCATION: 36
89           (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
90
91      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
92
93 Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
94 1               5                   10                  15
95 His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn Val Gly
96             20                  25                  30
97 Ser Asn Thr Tyr
98         35
99
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101    (2) INFORMATION FOR SEQ ID NO:3:
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103        (i) SEQUENCE CHARACTERISTICS:
104            (A) LENGTH: 37 amino acids
105            (B) TYPE: amino acid
106            (C) STRANDEDNESS: single
107            (D) TOPOLOGY: linear
108
109        (ii) MOLECULE TYPE: peptide
110
111        (ix) FEATURE:
112            (B) LOCATION: 2,7
113            (D) OTHER INFORMATION: disulfide bridge between
114                                   the Cys residues
115            (B) LOCATION: 37
116            (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
117
118
119        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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121    Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
122    1               5                   10                  15
123    Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Pro Ser Thr Asn Val
124            20                  25                  30
125    Gly Ser Asn Thr Tyr
126            35
127
128
129    (2) INFORMATION FOR SEQ ID NO:4:
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131        (i) SEQUENCE CHARACTERISTICS:
132            (A) LENGTH: 37 amino acids
133            (B) TYPE: amino acid
134            (C) STRANDEDNESS: single
135            (D) TOPOLOGY: linear
136
137        (ii) MOLECULE TYPE: peptide
138
139        (ix) FEATURE:
140            (B) LOCATION: 2,7
141            (D) OTHER INFORMATION: disulfide bridge between
142                                   the Cys residues
143            (B) LOCATION: 37
144            (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
145
146        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
147
148    Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
149    1               5                   10                  15
150    Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val
151            20                  25                  30
152    Gly Ser Asn Thr Tyr
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153                35
154
155
156    (2) INFORMATION FOR SEQ ID NO:5:
157
158         (i) SEQUENCE CHARACTERISTICS:
159              (A) LENGTH: 36 amino acids
160              (B) TYPE: amino acid
161              (C) STRANDEDNESS: single
162              (D) TOPOLOGY: linear
163
164       (ii) MOLECULE TYPE: peptide
165
166       (ix) FEATURE:
167              (B) LOCATION: 1,6
168              (D) OTHER INFORMATION: disulfide bridge between
169                                     the Cys residues
170              (B) LOCATION: 36
171              (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
172
173       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
174
175    Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
176    1               5                   10                  15
177    Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr Asn Val Gly
178                20                  25                  30
179    Ser Asn Thr Tyr
180                35
181
182
183    (2) INFORMATION FOR SEQ ID NO:6:
184
185         (i) SEQUENCE CHARACTERISTICS:
186              (A) LENGTH: 37 amino acids
187              (B) TYPE: amino acid
188              (C) STRANDEDNESS: single
189              (D) TOPOLOGY: linear
190
191       (ii) MOLECULE TYPE: peptide
192
193       (ix) FEATURE:
194              (B) LOCATION: 2,7
195              (D) OTHER INFORMATION: disulfide bridge between
196                                     the Cys residues
197              (B) LOCATION: 37
198              (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
199
200       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
201
202    Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
203    1               5                   10                  15
204    Val His Ser Ser Asn Asn Phe Gly Pro Val Leu Pro Pro Thr Asn Val
205                20                  25                  30
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206    Gly Ser Asn Thr Tyr
207            35
208
209
210    (2) INFORMATION FOR SEQ ID NO:7:
211
212        (i) SEQUENCE CHARACTERISTICS:
213            (A) LENGTH: 37 amino acids
214            (B) TYPE: amino acid
215            (C) STRANDEDNESS: single
216            (D) TOPOLOGY: linear
217
218        (ii) MOLECULE TYPE: peptide
219
220        (ix) FEATURE:
221            (B) LOCATION: 2,7
222            (D) OTHER INFORMATION: disulfide bridge between
223                                    the Cys residues
224            (B) LOCATION: 37
225            (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
226
227
228        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
229
230    Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu
231    1               5                   10                  15
232    Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val
233            20                  25                  30
234    Gly Ser Asn Thr Tyr
235            35
236
237    (2) INFORMATION FOR SEQ ID NO:8:
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239        (i) SEQUENCE CHARACTERISTICS:
240            (A) LENGTH: 36 amino acids
241            (B) TYPE: amino acid
242            (C) STRANDEDNESS: single
243            (D) TOPOLOGY: linear
244
245        (ii) MOLECULE TYPE: peptide
246
247        (ix) FEATURE:
248            (B) LOCATION: 1,6
249            (D) OTHER INFORMATION: disulfide bridge between
250                                    the Cys residues
251            (B) LOCATION: 36
252            (D) OTHER INFORMATION: amidated Tyr (Tyrosinamide)
253
254        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
255
256    Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe Leu Val
257    1               5                   10                  15
258    Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr Asn Val Gly
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/851,965*

INPUT SET: S28714.raw

Line	Error	Original Text
32	Wrong Classification	(C) CLASSIFICATION: Pending